

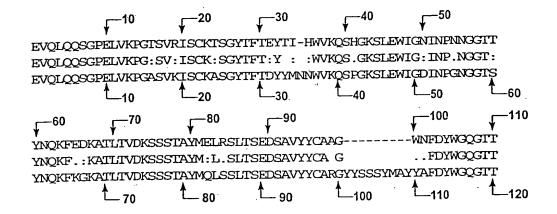
ENZYMES:

ALL 74 ENZYMES (NO FILTER)
LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE SETTINGS:

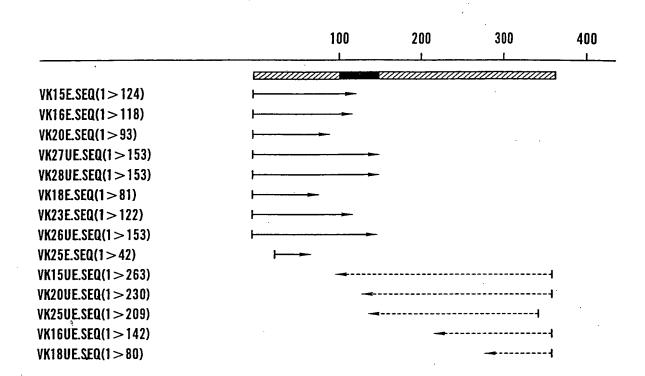
Ddel, Alu I Av	LI Eco57
Pst I Ava II Pvu II Sau	
SEO.ID.NO.1 TCTCCIGTCAGGAACIGCAGGIGICCTCTCTGAGGICCAGCTGCAACAGTCTGGAC	i i
├──	+++ ++++ 70:
SEQ.ID.NO.2 AGAGGACAGICCITGACGICCACAGGACACICCACGICGACGITGICACACCICG	
	'. T G E P E L V K
SEO.ID.NO.5 L S C Q E L Q V S S L R S S C N S L D	
Hph I	Dra III
Bsp6 II EcoR V	Bsrl
	דימריימיזמרימריזמרים
	''
SEQ.ID.NO.2 GCACCCIGAGICACTCCTATAGCACGITCTGAAGACCTATGTGTAAGTGACTTAT SEQ.ID.NO.3 A W D F S E D I L Q D F W I H I H . I	AIGGIAIGIGACCC Y H T L G
SEO.ID.NO.4 P G T S V R I S C K T S G Y T F T E Y	
SEQ.ID.NO.5 LGLQ.GYPARLLDTHSLN	T P Y T G
Hph I	Rsal
Nco I	Kpn I
SEQ.ID.NO.1 TGAAGCAGCCATGGAAAGAGCCTTGAGTGGATTGGAAACATCAATCCTAACAAT	GGIGGIACCACCIA
SEQ. ID.NO.2 ACTTOGICTOGGIACCITTICTOGGAACICACCITAGCITTIGIAGTTAGGAITGITA	CCACCATGGTGGAT
0DQ.1D.110.5 2 11 = 1 11 11 = 1 1	WWYHL
SEQ.ID.NO.4 V K Q S H G K S L E W I G N I N P N N SEO.ID.NO.5 · S R A M E R A L S G L E T S I L T M	
SEQ.ID.NO.5 · S R A M E R A L S G L E T S I L T M	Alu l
•	
Bsr I	Ban II
Taq I Hae III Acc I Rsa I	Sac
Taq I Hae III Acc I Rsa I SEO. TD. NO. 1 CAATCAGAAGITOGAGGACAAGGCCACATTGACTGTAGACAAGTCCTCCAGTACAG	Sac CCTACATGGAGCTC
Taq I Hae III Acc I Rsa I	Sac I CCTACATGGAGCTC +++ +++ 280
SEQ. ID.NO.1 CAATCACAAGITCGAGGACAAGCCCACATTGACIGIAGACAAGICCTCCAGIACAGGSEQ. ID.NO.2 GITAGICITCAAGCICCIGITCGAGGIGIAACIGACATCIGITCAAGCACGICATGICCAGGICATGICCAGGICATGICCAGGICAAGICCTCAAGCICCTGTTCCGGIGIAACIGACATCIGITCAAGCACGICATGICCAGGICATGICCAGGICAAGICCTGTTCAGGAGGICATGICCAGGICAAGICCTGTTCAGGAGGICATGICCAGGICAAGICCTGTTCAGGAGGICATGICCAGGICAAGICCTGTTCAGGAGGICATGICCAGGICAAGICCTGTTCAGGAGGICATGICCAGGICAAGICCTGTTCAGGAGGICATGICCAGGICAAGICCTGTTCAGGAGGICATGICCAGGICAAGICCTGTTCAGGAGGICATGICCAGGICAAGICCTCAGGICAAGICCTCAGGICAAGICCTCAGGICAAGICCTCAGGICAAGICCTCAGGICAAGICCTCAGGICAAGICCTCAGGICAGGI	Sac I CCTACATGGAGCTC HILLHHILLH 280 GGATGTACCTCGAG L H G A
SEQ.ID.NO.1 CAATCACAAGITCCACCACAACCCCACATTCACIGIAGACAAGICCICCAGIACAG SEQ.ID.NO.2 GITAGICITCAAGCICCIGITCCCGIGIAACIGACATCIGITCACCACGICATGIC SEQ.ID.NO.3 Q S E V R G Q G H I D C R Q V L Q Y S SEQ.ID.NO.4 N Q K F E D K A T L T V D K S S S T	Sac I CCTACATGGAGCTC HILLHILL 280 CGATGTACCTCGAG L H G A A Y M E L
SEQ. ID.NO.1 CAATCACAAGTTCCAGGACAAGCCCACATTGACTGTAGACAAGTCCTCCAGTACAGGSEQ. ID.NO.2 GTTAGTCTTCAAGCTCCTGTTCCGGTGTAACTGACATCTGTTCAGGACGACGTCATGTCCGGTGTAACTGACATCTGTTCAGGACGACGTCATGTCCGGTGTAACTGACATCTGTTCAGGACGTCATGTCCGGTTCAGGACGTCATGTCCGGTTCAGGACGTCATGTCCGGTTCAGGACGTCATGTCCGGTTCAGGACGTCATGTCCGGTTCAGGACGTCATGTCCGGTTCAGGACGTCATGTCCGGTTCAGGACGTCATGTCCGGTTCAGGACGTCATGTCCGGTTCAGGACGTCATGTCCGGTTCAGGACGTCATGTCCGGTTCAGGACGTCATGTCCGGTTCAGGACGTCATGTCCGGTTCAGGACGTCATGTCCGGTTCAGGACGTCATGTCCGGTTCAGGACGACGTCATGTCCGGTTCAGGACAAGTCCTCCAGTTCAGGACAAGTCCTCCAGGTCATGTCCGGTTCAGGACAAGTCCTCCAGGTACAGGTCATGTCCGGTTCAGGACAAGTCCTCCAGGTCATGTCCGGTTCAGGACAAGTCCTCCAGTACAGGTCATGTCCAGGTCATGTCCAGGTCATGTCCAGGTCAGGACAAGTCCTCCAGGTACAGGACAAGTCCTCCAGGTACAGGACAAGTCCTCCAGGTACAGGACAAGTCCTCCAGGTACAGGACAAGTCCTCCAGGTACAGGACAAGTCCTCCAGGTACAGGACAAGTCCTCCAGGTACAGGACAAGTCCTCCAGGTACAGGACAAGTCCTCCAGGTACAGGACAAGTCCTCCAGGTACAGGACAAGTCCTCCAGGTACAGGACAAGTCCTCCAGGTACAGGACAAGTCCTCCAGGTACAGGACAAGTCCTCAGGTACAGGACAAGTCCTCAGGTACAGGACAAGTCCTCAGGTACAGGACAAGTCCTCAAGTACAGGACAAGTCCTCAAGTACAGGACAAGTCCTCAAGTACAGGACAAGTCCTCAAGTACAGGACAAGTCCTCAAGTACAGGACAAGTCCTCAAGTACAGGACAAGTCCTCAAGTACAGGACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCCTCAAGTACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTACAAGTCAAGTCAAGTCAAGTACAAGTCAAGTCAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTACAAGTCAAGTACAAGTCAAGTCAAGTACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTACAAGTCAAGTACAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTAAAAGTCAAGTAAAAGTCAAGTCAAGTAAAAAAAGTCAAGTACAAGTCAAAGTCAAGTAAAAAAAA	Sac I CCTACATGGAGCTC HILLHHILLH 280 GGATGTACCTCGAG L H G A
SEQ.ID.NO.1 CAATCACAAGITCCACCACAACCCCACATTCACIGIAGACAAGICCICCAGIACAG SEQ.ID.NO.2 GITAGICITCAAGCICCIGITCCCGIGIAACIGACATCIGITCACCACGICATGIC SEQ.ID.NO.3 Q S E V R G Q G H I D C R Q V L Q Y S SEQ.ID.NO.4 N Q K F E D K A T L T V D K S S S T	Sac I CCIACATGGAGCIC HILLIHI 280 GGATGTACCTGGAG L H G A A Y M E L P T W S S Sau96 I
SEQ. ID.NO.1 CAATCAGAAGITOGAGGACAAGGCCACATTGACIGIAGACAAGICCTCCAGIACAG SEQ. ID.NO.2 GITAGICITCAAGCICCIGITCCGGIGIAACIGACACATCIGITCAGCAGGICATGIC SEQ. ID.NO.3 Q S E V R G Q G H I D C R Q V L Q Y S SEQ. ID.NO.4 N Q K F E D K A T L T V D K S S S T SEQ. ID.NO.5 T I R S S R T R P H . L . T S P P V Q	Sac Sac
Taq Hae	Sac CCIACATGGAGCIC H
SEQ. ID.NO.1 CAATCAGAAGITOGAGGACAAGGCCACATTGACIGIAGACAAGICCTCCAGIACAG SEQ. ID.NO.2 GITAGICITCAAGCICCIGITCCGGIGIAACIGACAAGICCTCCAGIACAG SEQ. ID.NO.3 Q S E V R G Q G H I D C R Q V L Q Y S SEQ. ID.NO.4 N Q K F E D K A T L T V D K S S S T SEQ. ID.NO.5 T I R S S R T R P H . L . T S P P V Q Dde Hinf Pst	Sac CCTACATGGAGCTC H
SEQ. ID.NO.1 CAATCAGAAGITOGAGGACAAGGCCACATTGACIGIAGACAAGICCTCCAGTACAG SEQ. ID.NO.2 GITAGICITCAAGCICCIGITCCGGIGIAACIGACAAGICCTCCAGTACAG SEQ. ID.NO.3 Q S E V R G Q G H I D C R Q V L Q Y S SEQ. ID.NO.4 N Q K F E D K A T L T V D K S S S T SEQ. ID.NO.5 T I R S S R T R P H . L . T S P P V Q Dde Hinf Pst Pvu SEQ. ID.NO.1 CGCAGCCTAACATCIGAGGATTCTGCAGGICTATTATTGTGCAGCTGGTTGGAACTT HILLIAG HINF HILLIAG HINF HILLIAG SEQ. ID.NO.2 GCGICGGATTGTAGACTCCTAAGACGTCAACATCTTGAA	Sac CCTACATGGAGCTC H
SEQ. ID.NO.1 CAATCACAAGITCCACGACAAGCCCACATTGACIGIAGACAAGICCTCCAGTACAGGID.NO.2 GITAGICITCAAGCICCIGITCCGGIGIAACTGACATCIGITCAGGACGICATGICCGGID.NO.3 Q S E V R G Q G H I D C R Q V L Q Y S SEQ. ID.NO.4 N Q K F E D K A T L T V D K S S S T SEQ. ID.NO.5 T I R S S R T R P H . L . T S P P V Q A SEQ. ID.NO.1 CGCAGCCTAACATCIGAGGATCTTTTTTTTTTTTTTTTTT	Sac CCTACATGGAGCTC HI HI HI 1280 CCATGTACCTCGAG L H G A A Y M E L P T W S S Sau96 Bsr Hae TGACTACTGGGGCC HI HI HI HI 1350 ACTGATGACCCGGG L L G P
Taq Hae	Sac CCTACATGGAGCTC HI HI HI 1280 CCATGTACCTGGAG L H G A A Y M E L P T W S S Sau96
Taq Hae	Sac CCTACATGGAGCTC HI HI HI 1280 CCATGTACCTGGAG L H G A A Y M E L P T W S S Sau96
Taq! Hae	Sac CCTACATGGAGCTC HI HI HI 1280 CCATGTACCTGGAG L H G A A Y M E L P T W S S Sau96
Taq	Sac CCTACATGGAGCTC HI HI HI 1280 CCATGTACCTGGAG L H G A A Y M E L P T W S S Sau96
Taq! Hae	Sac CCTACATGGAGCTC HI HI HI 1280 CCATGTACCTGGAG L H G A A Y M E L P T W S S Sau96
SEQ. ID.NO.1 CAATCAGAAGITCGAGGACAAGCCCACATTGACTGTAGACAAGTCCTCCAGTACAG SEQ. ID.NO.2 GTTAGTCTCAAGCCCCTGTTCCCGTGTACACACTCTGTCACACAGTCCTCCAGTACAG SEQ. ID.NO.3 Q S E V R G Q G H I D C R Q V L Q Y S SEQ. ID.NO.4 N Q K F E D K A T L T V D K S S S T SEQ. ID.NO.5 T I R S S R T R P H . L . T S P P V Q Dde Hinf Pst Pvu Pvu	Sac CCTACATGGAGCTC H
Taq Hae	Sac CCTACATGGAGCTC HI HI HI 1280 CCATGTACCTGGAG L H G A A Y M E L P T W S S Sau96

LIPMAN-PEARSON PROTEIN ALIGNMENT KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>115)	SEQ2(1>125)	SIMILARITY	GAP	GAP	CONSENSUS
J591VH.PRO	MUVHIIA.PRO		NUMBER	LENGTH	LENGTH
(1>115)	(1>125)	75.6	2	10	125



LTVSS :TVSS VIVSS



ALL 74 ENZYMES (NO FILTER): **ENZYMES:** LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE **SETTINGS:** Hphl TTATATGAGCTGATGGGAACATTGTAATGACCCAATCTCCCAAATCCATGTCCATGTCAGTAGAGACAT SEO.ID.NO.9 SEQ. ID. NO. 10 AATATACCTOGACTACCCTTGTAACATTACTGGGTTAGAGGGTTTAGGTACAGGTACAGTCATCCTCTCT SEO.ID.NO.11 L Y G A D G N I V M T Q S P K S M S M S V G E P C SEQ.ID.NO.12 WEHCNDPIS I W S R. SEQ.ID.NO.13 I Hae III Bsrl GGGTCACCTTGACCTGCAAGGCCAGTGAGAATGTGGTTACTTATGTTTCCTGGTATCAACAGAAACCAGA SEQ.ID.NO.9 SEQ.ID.NO.10 CCCAGTGGAACTGGACGTTCCGGTCACTCTTACACCAATGAATACAAAGGACCATAGTTGTCTTTGGTCT SEO.ID.NO.11 R V T L T C K A S E N V V T Y V S W Y Q Q K P E SEQ.ID.NO.12 G S P . P A R P V R M W L L M F P G I N R N O SEQ.ID.NO.13 G H L D L Q G Q . E C G Y L C F L V S T E T R Mbo I Ava II |Dpn I Bsr I |Hpa II Bsa0 I Sau96 1 Rsa I Alw26 I Fok I lPvu I GCAGTCTCCTAAACTCCTCATATACCCCCCATCCAACCCCGTACACTCCCCCCATCCCCTTCACACCC SEQ. ID.NO. 9 SEQ.ID.NO.10 OGTCAGAGGATTTCACGACTATATGCCCCGTAGGTTGGCCATGTGACCCCAGGGGCTAGCGAAGTGTCCG Q S P K L L I Y G A S N R Y T G V P D R F T G SEO.ID.NO.11 SEQ.ID.NO.12 S S L L N C . Y T G H P T G T L G S P I A S Q A RGI V Ρ H. SEQ.ID.NO.13 A V S Mbo I Eco57 I Mbo II Bsp6 II Dpn I AGTGGÁTCTGCAACAGATTTCACTCTGACCATCAGCAGTGTGCAGGCTGAAGACCTTGCAGATTATCACT SEQ.ID.NO.9 SEQ.ID.NO.10 TCACCTAGACGITGICTAAAGICAGACTGGTAGTCGTCACACGTCCGACTTCTGGAACGTCTAATAGTGA SEQ.ID.NO.11 S G S A T D F T L T I S S V Q A E D L A D Y H V D L Q Q I S L . P S A V C R L K T SEQ.ID.NO.12 SEQ.ID.NO.13 Q W I C N R F H S D H Q Q C A G . R P C R L S Ava II Sau96 I Alu I | Alu I |Rsa | GTGCACAGGTTACAGCTATCCGTACAGGTTCGGAGGGGGGCCCAAGCTGCAAATAAAACGGGCTGATGC SEQ.ID.NO.9 SEQ.ID.NO.10 CACCIGICCCAAIGICGATAGGCAIGIGCAAGCCICCCCCCIGGITCGACCITTATTITGCCCGACIACG SEQ.ID.NO.11 C G Q G Y S Y P Y T F G G G T K L E I K R A D A SEQ.ID.NO.12 V D R V T A I R T R S E G G P S W K . NGLM G D G SEQ.ID.NO.13 TGCACCAACTGTA SEO.ID.NO.9 SEQ.ID.NO.10 ACGIGGITGACAT APTV SEQ.ID.NO.11 SEQ.ID.NO.12 L H Q L Y SEQ.ID.NO.13 C T N C FIG. 10



LIPMAN-PEARSON PROTEIN ALIGNMENT KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>107) J591VK.PRO	SEQ2(1 > 1 1 1) MUVKV.PRO	SIMILARITY INDEX	GAP NUMBER	GAP LENGTH	CONSENSUS LENGTH
(1>107)	(1>109)	60.4	2	2	109
↓ ^{—10}	20	†	40 🕌 5	•	

